

Claims:

1. A method for altering a characteristic or state of a cell comprising:
  - treating a first cell type with an agent capable of altering a characteristic or state in a cell; and
5. determining the degree of alteration in the treated cell by measuring a methylation signature within the genome of the treated cell, wherein a given methylation signature is indicative of an altered characteristic or state of the treated cell.
2. The method according to claim 1 wherein the first cell type is selected from the group consisting of a cell derived from an individual suffering from age-related disabilities, a disease such as cancer, an autoimmune disease, cardiovascular problems such as myocardial infarction or ischemia, stem cell, T cells or monocytes of the immune and hematopoietic system, normal, and mixtures thereof.
10. 3. The method according to claim 2 wherein the first cell type is a stem cell.
4. The method according to any one of claims 1 to 3 wherein the agent is selected from the group consisting of a chemical, drug, nucleic acid, aptamer, antibody, antigen, intercalating nucleic acid (INA), peptide nucleic acid (PNA), Locked Nucleic Acid (LNA), Hexitol Nucleic Acid (HNA), Altritol Nucleic Acid (ANA), Cyclohexanyl Nucleic Acid (CNA), oligonucleotide, modified oligonucleotide, single stranded DNA, RNA, protein, peptide, an extract, lysate or cellular component from a second cell type
15. 20. having a desired characteristic or state, a combination thereof, and chimeric versions thereof.
5. The method according to claim 4 where the agent is an extract, lysate or cellular component from a second cell type having a desired characteristic or state.
6. The method according claim 5 wherein the second cell type is any cell type or
25. combination of cell types.
7. The method according claim 6 wherein the first and second cell types are selected from the group consisting of cells of the human haematopoietic system, other stem cells, and epithelial cells.
8. The method according claim 7 wherein the second cell type is derived from a normal
30. or healthy individual of a cell type similar to the first cell type.
9. The method according claim 8 wherein the second cell type is a stem cell.

10. The method according to any one of claims 1 to 9 wherein the first cell type cell and the second cell type cell are of the same cell type from the same species.
11. The method according to any one of claims 1 to 9 wherein the first cell type and the second cell type are not of the same cell type.
- 5 12. The method according to any one of claims 1 to 9 wherein the first cell type and the second cell type are not of the same species.
13. The method according to claim 12 wherein the second cell type is an amphibian cell and the first cell type is human or other mammalian cell.
14. The method according to any one of claims 1 to 13 wherein the first cell type is pre-treated so as to make the cell permeable to macromolecules.
- 10 15. The method according to claim 14 wherein the cell is pre-treated by electroporation, low temperature thermal shock, or various enzymes such as streptolysin O.
16. The method according to claim 15 wherein the pre-treatment renders the cell temporally permeable.
- 15 17. The method according to any one of claims 1 to 16 further including:  
culturing or growing the treated cell to obtain multiple copies of the treated cell.
18. The method according to claim 17 wherein the treated cell is cultured in any suitable media or host under conditions that are suitable for cell growth and division.
19. The method according to claim 18 wherein the host is a domestic animal selected  
20 from the group consisting of bovine, ovine, equine, poultry, and porcine.
20. The method according to any one of claims 1 to 19 wherein the methylation signature is a group of cytosines within a region of the genome that has a characteristic methylation signature which corresponds to a specific cell type.
21. The method according to any one of claims 1 to 20 wherein the methylation  
25 signature is determined by the bisulphite modification and subsequent DNA sequence analysis.